

Smokescreen™ Genotyping Array

The Premier Array for Addiction Research

Designed specifically for researchers interested in the causes and treatment of addiction

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We began by conducting a study of the cutting-edge research available on addiction, in collaboration with leading addiction research scientists, and then assembling a list of genetic variants. Next, with support from the United States National Institute on Drug Abuse, we designed Smokescreen™ to support a wide variety of research goals related to addiction, smoking cessation, drug response, and consequences of smoking. Since its release, Smokescreen™ has quickly become the premier genotyping array for addiction research, and already about 100,000 Smokescreen™ arrays have been used by researchers worldwide. If you have any questions or comments, please let us hear from you! We'll be happy to help.



But we don't just make arrays; since we are addiction researchers ourselves, and we researched and designed Smokescreen™, we also have the most experience when it comes to its use and analyzing its results. Let us hear from you so we can help you avoid common pitfalls, learn the best practices, and get the highest quality results. For example, here are a few of the services we offer that can help:

- Quality control, phasing, and imputation
- Genome-wide association scans
- Biomarker predictions and polygenic risk modeling

We even offer free email and telephone consultations to help you get started or to decide if Smokescreen™ is the right choice for your project!

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BioRealm, LLC · 340 S Lemon Ave · Suite 1931 · Walnut, CA 91789-2706 · United States
+1 (855) 777-3256 · smokescreen@biorealm.ai · <https://biorealm.ai>

Highlights

More addiction-related content than any other commercially available array:

- Covers 98% of common genetic variation in 1000+ addiction genes
- More than 296K markers, selected for African, East Asian, and European populations
- More than 20K markers from expert nomination, knowledge-bases, candidate gene arrays, and the literature

Better genome-wide imputation coverage of common variants than most similarly-sized arrays:

- African (66%), East Asian (82%), and European (91%)

More nicotine and tobacco-related content than any other commercially available array:

- More than 11K markers in the nicotine acetylcholine receptor gene cluster (CHRNA5-CHRNA3-CHRNA4) and nicotine metabolizer regions (CYP2A6-CYP2B6)
- More than 16K markers for related co-morbidities and diseases
- Dense coverage of 1014 addiction genes identified through expert nomination, and recent bioinformatics projects and knowledge-bases
- 8948 SNPs and indels (average of one marker per 62 base pairs) were selected for the 552 kb LD block encompassing the chr15q25.1 nicotinic acetylcholine receptor (nAChR) gene cluster (CHRNA5, CHRNA3 and CHRNA4)
- For CYP2A6 (± 20 kb), 612 markers were selected with an average of one marker every 75 base pairs
- For CYP2B6 (± 20 kb), 1628 markers were selected with one marker per 45 base pairs on average
- Additional markers were selected to capture variation in the surrounding region, including EGLN2, CYP2A7, CYP2G1P, and CYP2B7P1
- 2271 markers from the candidate gene/pathway arrays developed and used by the Pharmacogenetics of Nicotine Addiction Treatment (PNAT) research program [1, 2]
- 3091 markers from a lung cancer meta-GWAS [3]
- 1200 markers related to psychiatric comorbidities from the Psychiatric Genetics Consortium [4]
- 7956 and 2247 markers for pulmonary and cardiovascular phenotypes respectively from the UK Biobank Axiom Array [5]
- 1329 markers related to addiction identified in recent literature from NIDA Genetics Consortium investigators
- 12,058 markers used in the smoking-cessation v1.0 Quit Success Score biomarker [6]
- 2030 pharmacogenomic markers related to absorption, distribution, metabolism, and excretion (ADME)
- 7612 markers identified in previous genome-wide association studies or addiction and related diseases [7]
- Validated in laboratory studies of nicotine metabolism.

Frequently Asked Questions

- **How can I download the complete set of Smokescreen™ genotyping array annotations?**

Please get in touch with us via email or telephone and we'll be happy to provide them.

- **Where can I read more about Smokescreen™?**

See our original article describing Smokescreen™ linked in the next answer below.

- **How should I cite Smokescreen™ in a published work?**

We prefer that our original article describing Smokescreen™ be used for this purpose:

Baurley, J.W., Edlund, C.K., Pardamean, C.I., Conti D.V., Bergen A.W. Smokescreen: a targeted genotyping array for addiction research. BMC Genomics 17, 145 (2016).

<https://doi.org/10.1186/s12864-016-2495-7>

<https://www.biomedcentral.com/1471-2164/17/145>

<https://web.archive.org/web/20200229211603/https://www.biomedcentral.com/1471-2164/17/145>

Smokescreen™ Categorized Marker Count Summary

Category	Marker Count ¹
1014 Addiction-related Genes ²	
Tag SNPs (MAF ≥ 0.05)	255,862
Exonic Markers	17,632
Genome-wide Association Markers	
Affymetrix' Axiom® Biobank GWAS Grid	246,038
African (YRI) Booster Panel	50,000
Fine-mapping Of Smoking Related Loci	
CHRNA5-CHRNA3-CHRNA4 (552 kb LD Block)	8,913
CYP2A6 (±20 kb)	573
CYP2B6 (±20 kb)	1,613
High-value Addiction Markers	
NeuroSNP Project	4,994
Pharmacogenetics of Nicotine Addiction Treatment (PNAT) SNP Panels	2,271
v1.0 Quit Success Score	12,058
Literature Search	1,329
Comorbidity Markers	
Lung Cancer	3,091
Psychiatric Disorders	1,200
Tobacco Smoke Constituent Update And Metabolic Phenotypes	1,907
Pulmonary Diseases And Traits	7,945
Cardiovascular Diseases And Traits	2,247

¹ There may be some unavoidable marker count overlap between categories.

² [Smokescreen™ addiction regions and estimated imputed coverage](#). See this file for addiction-related gene regions (chr 1–22) represented on the Smokescreen™ array and the estimated imputation-based coverage for each region in European (EUR), Asian (ASN), and African (YRI) populations. (ODS 332.9 KB)

General High-value Markers		
	Pharmacogenomic Markers	2,030
	Nhgri Gwas Catalog	7,612
	Eqtls	9,736
	Loss-of-function Markers	4,680
	Ancestry Informative Markers (Aims)	5,545
	HLA/KIR	8,894
	Mitochondrial	180
Total		646,247

References

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3. Bahcall O, Orli B. COGS project and design of the iCOGS array. *Nat Genet.* 2013;45(4):343. doi:10.1038/ng.2592.
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7. A Catalog of Published Genome-Wide Association Studies <https://www.genome.gov/gwastudies>. Accessed 20 Nov 2015.